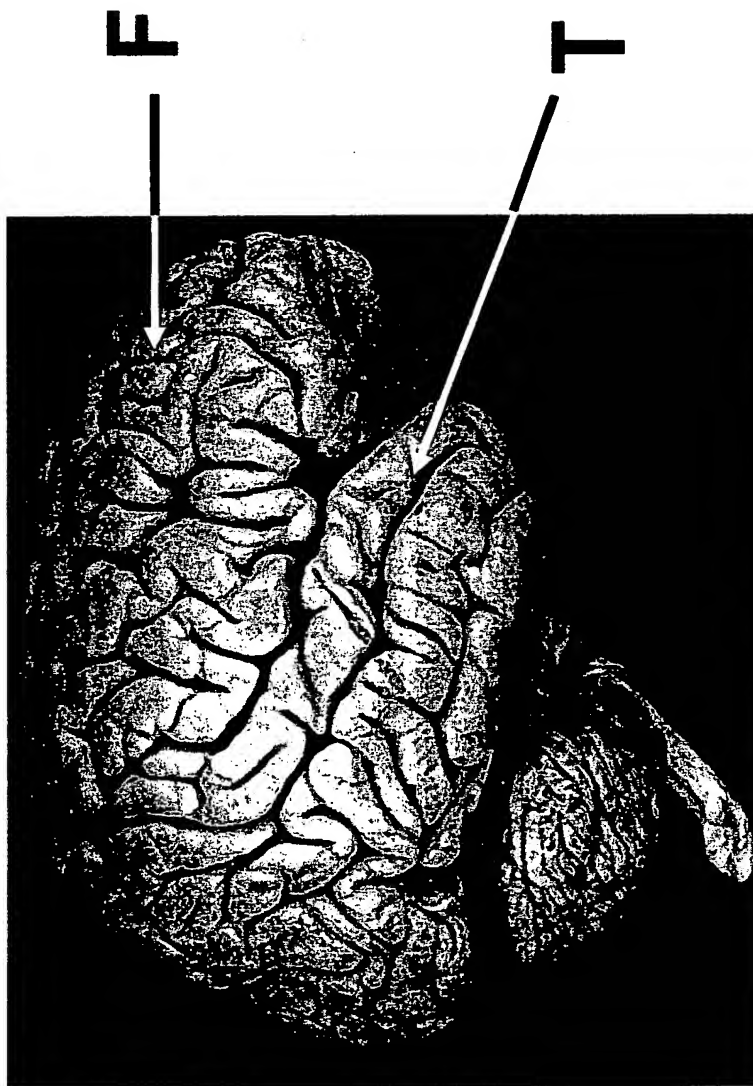


-1/26-

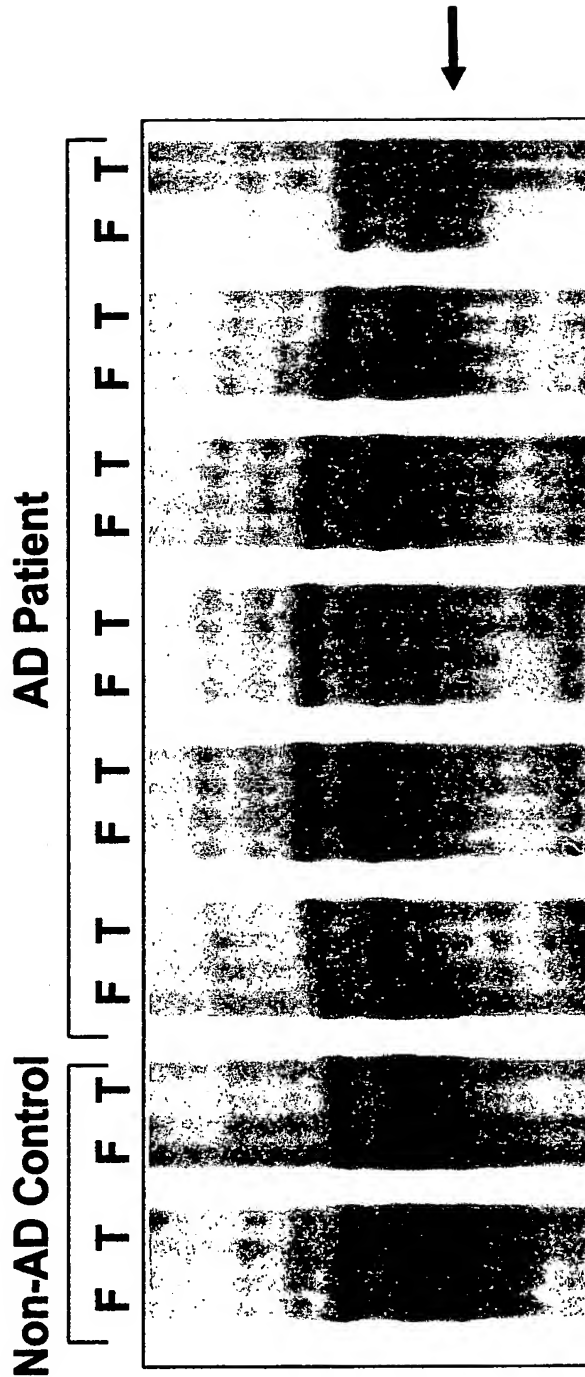
**Fig. 1: Identification of Genes Involved  
in Alzheimer's Disease Pathology**



Best Available Copy

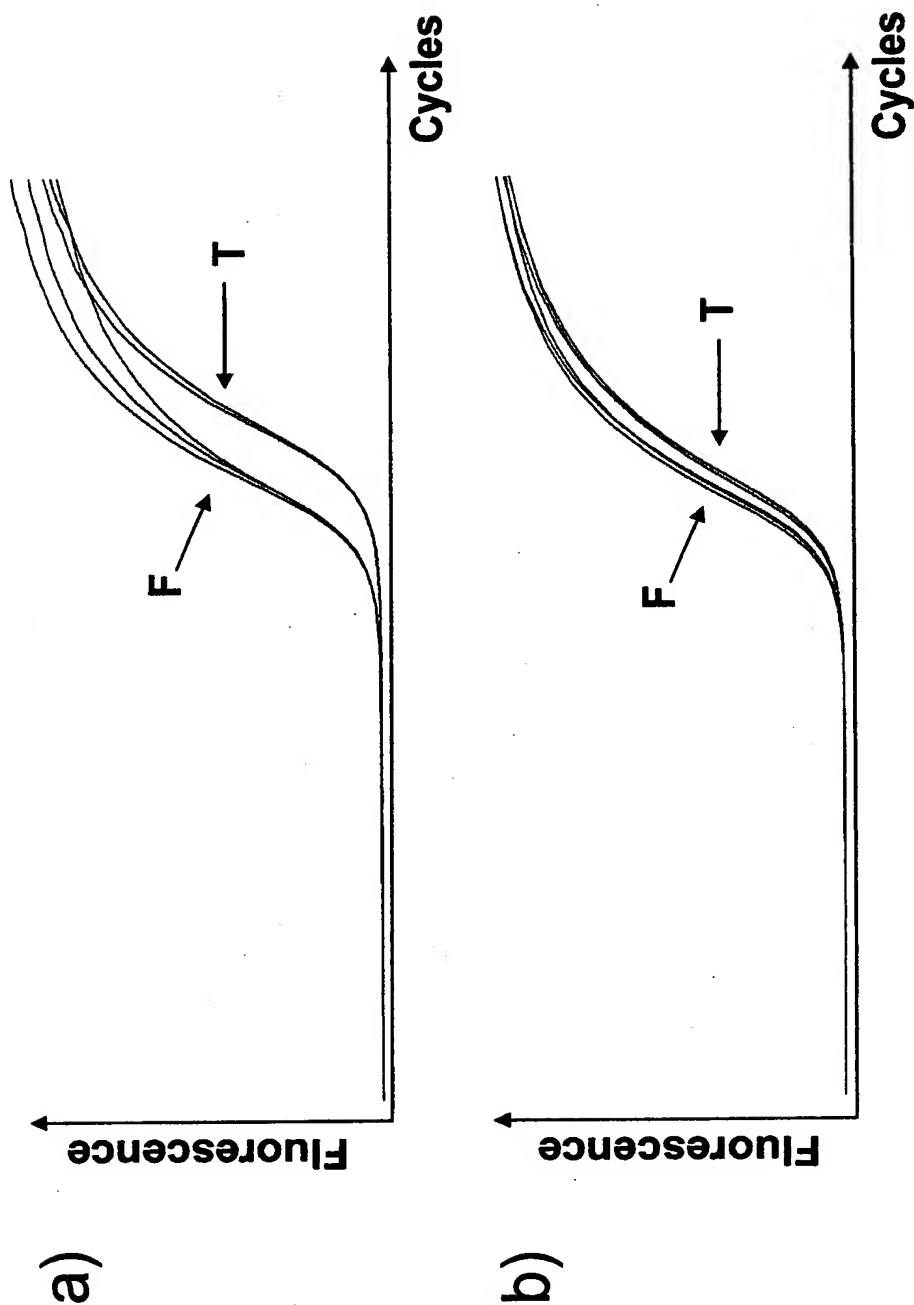
-2/26-

**Fig. 2: Identification of differentially expressed genes in a fluorescence differential display screen**



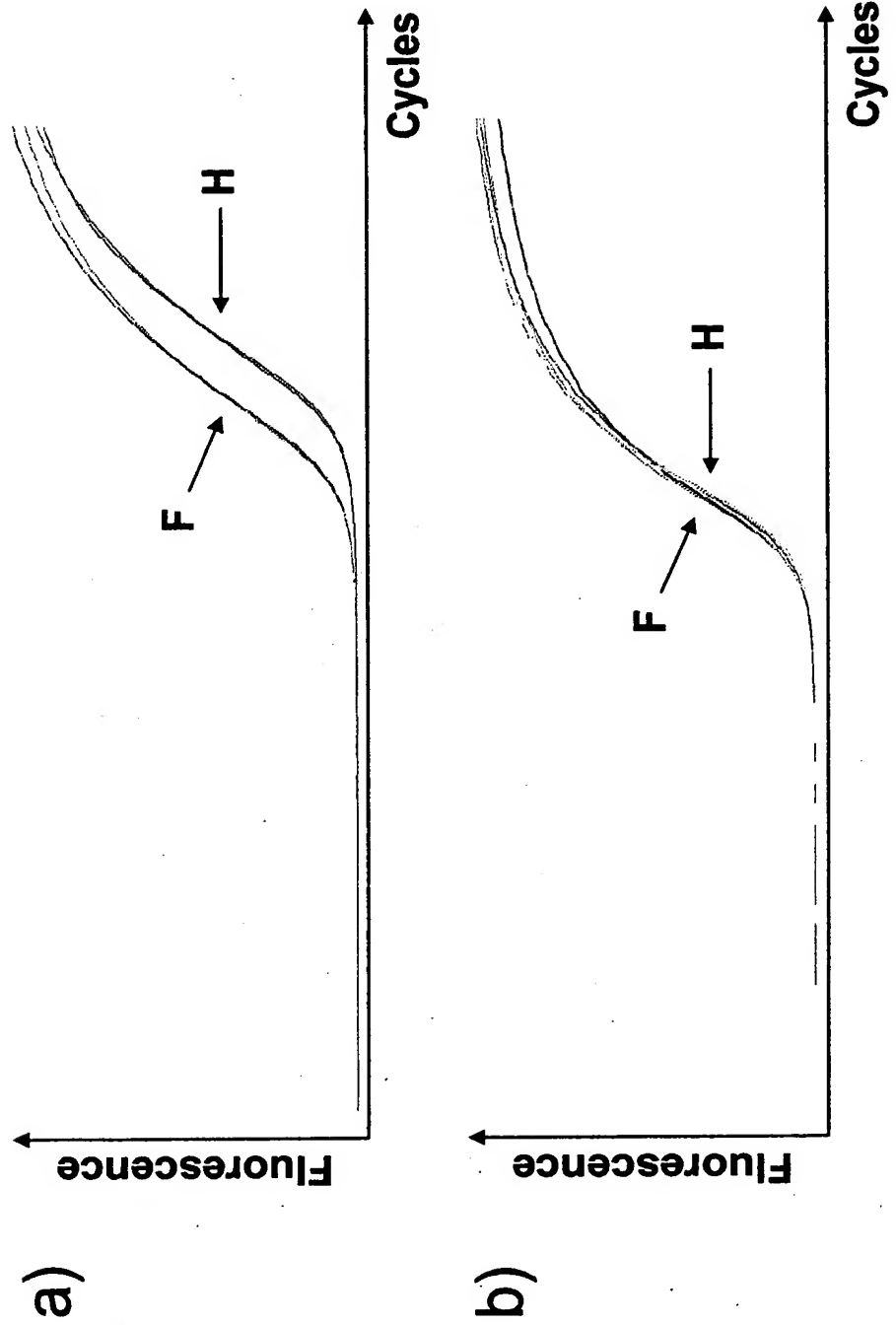
-3/26-

**Fig. 3: Verification of differential expression of human MAGUIN-1 by quantitative RT-PCR**



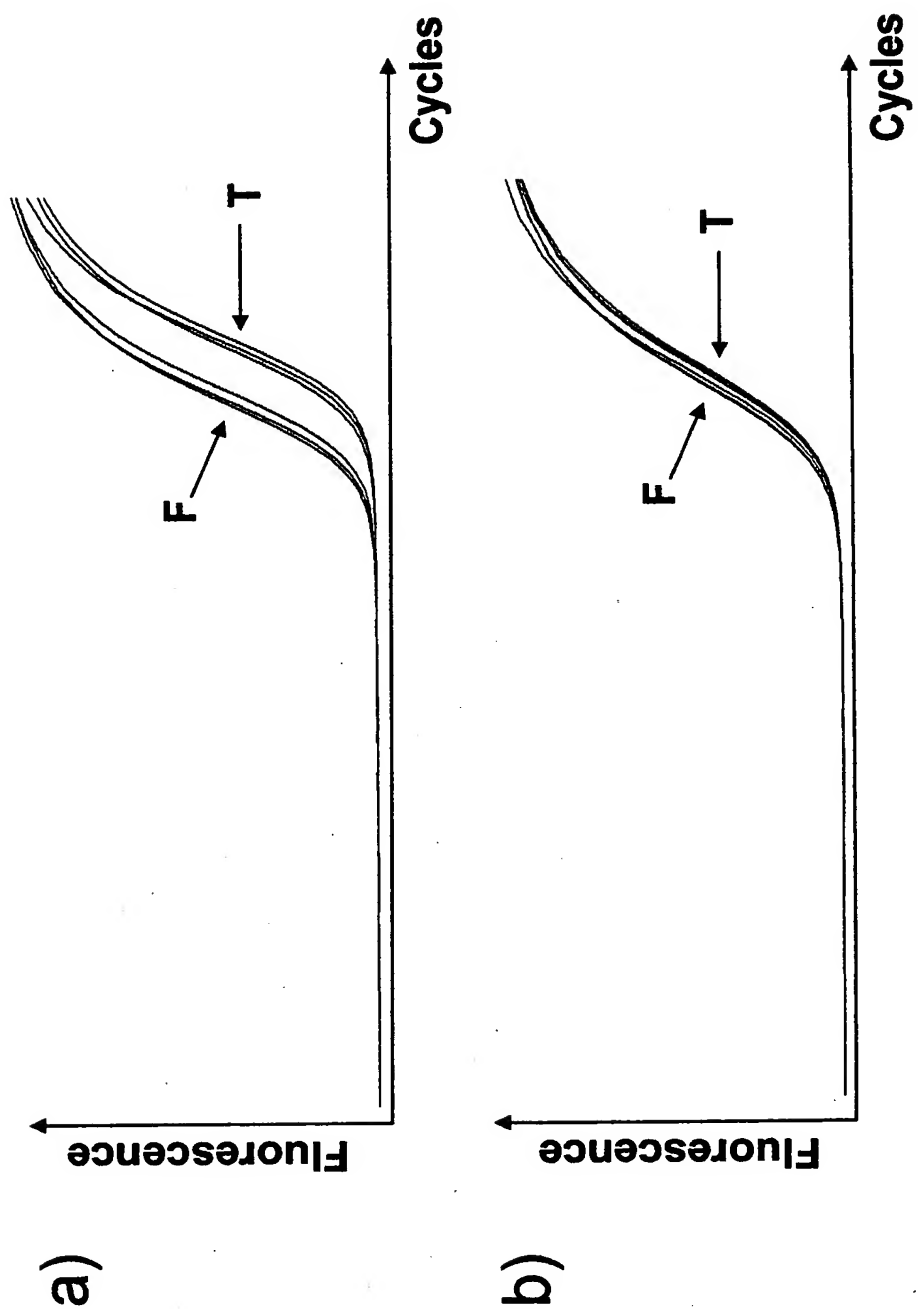
-4/26-

**Fig. 4: Verification of differential expression of Maguin-1 by quantitative RT-PCR**



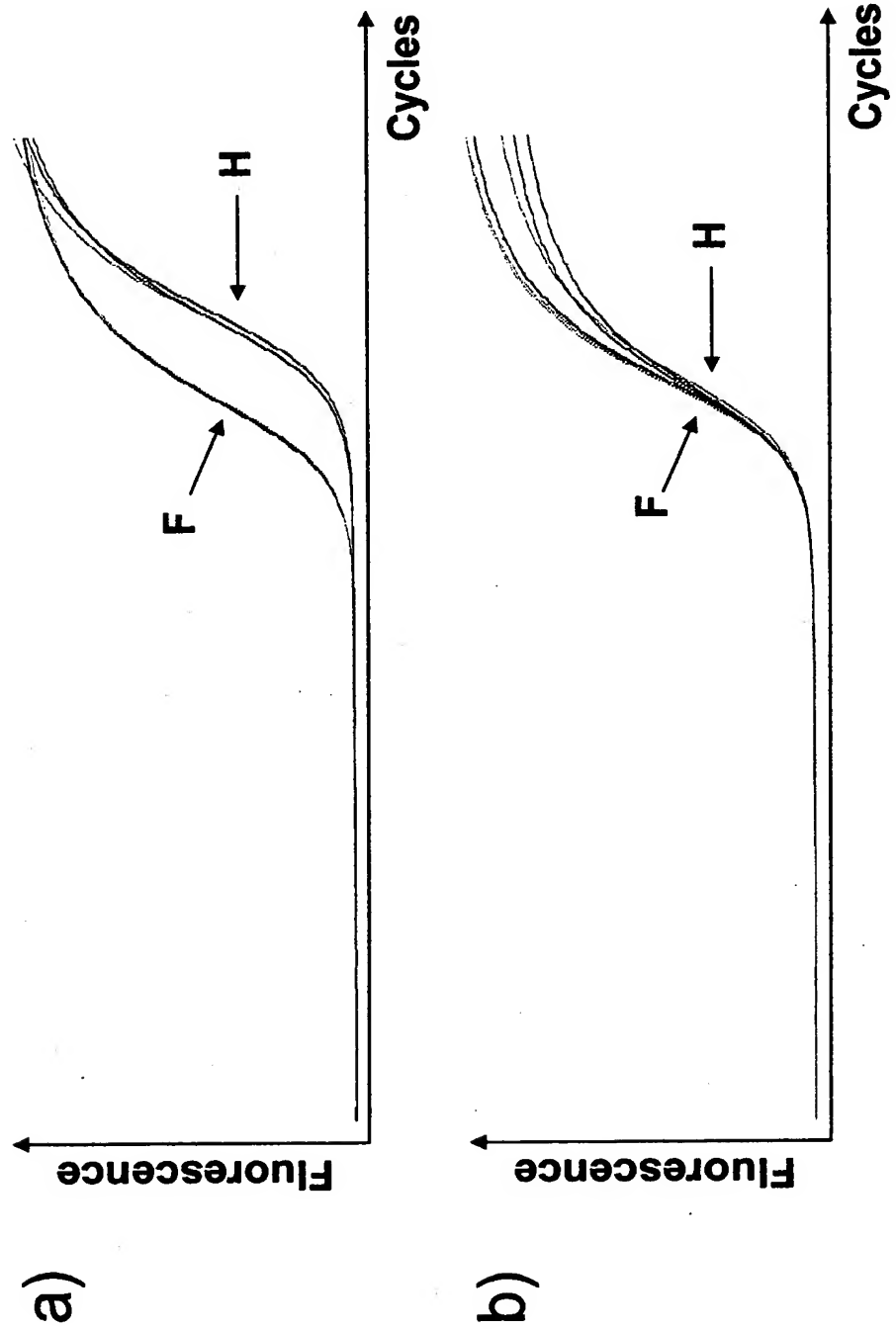
-5/26-

**Fig. 5: Verification of differential expression of human MAGUIN-2 by quantitative RT-PCR**



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**Fig. 6: Verification of differential expression of Maguin-2 by quantitative RT-PCR**



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**Fig. 7: SEQ ID NO. 1:  
amino acid sequence of  
human MAGUIN-1 protein**

**Length: 1034 aa**

1 MALIMEPVSK WSPSQVVDWM KGLDDCLQQY IKNFEREKIS GDQLLRITHQ  
51 ELEDLGVSRI GHQELILEAV DLLCALNYGL ETENLKTLSH KLNASAKNLQ  
101 NFITGRRRSRSG HYDGRTSRKL PNDFLTSVVD LIGAAKSLLA WLDRSPFAAV  
151 TDYSVTRNNV IQLCLELTTI VQQDCTVYET ENKILHVCKT LSGVCDHIIS  
201 LSSDPLVSQS AHLEVIQLAN IKPSEGLGMY IKSTYDGLHV ITGTTENSPA  
251 DRCKKIHAGD EVIQVNHQTV VGWQLKNLVN ALREDPSGVI LTLKKRPQSM  
301 LTSAPALLKN MRWKPLALQP LIPRSTSSV ATPSTISTP TKRDSSALQD  
351 LYIPPPPAEP YIPRDEKGNL PCEDLRGHMV GKPVHKGSES PNSFLDQEYR  
401 KRFNIVEEDT VLYCYEYKRG RSSSQGRRES TPTYGKLRLPI SMPVEYNWVG  
451 DYEDPNKMKR DSRRENSLLR YMSNEKIAQE EYMFQRNSKK DTGKSKKKKG  
501 DKSNSPTHYS LLPSLQMDAL RQDIMGTPVP ETTLYHTFQQ SSLQHKSXXX  
551 NKGPIAGKSK RRISCKDLGR GDCEGWLWKK KDAKSYFSQK WKKYWFLVKD  
601 ASLYWYINEE DEKAEGFISL PEFKIDRASE CRKKYAFKAC HPKIKSFYFA  
651 AEHLDDMNRLW LNRINMLTAG YAERERIKQE QDYWSESDKE EADTPSTPKQ  
701 DSPPPPYDTY PRPPSMSCAS PYVEAKHSRL SSTETSQSQS SHEEFRQEV  
751 GSSAVSPIRK TASQRRSWQD LIETPLTSSG LHYLQTLPLE DSVFSDSAAI  
801 SPEHRRQSTL PTQKCHLQDH YGPYPLAESE RMQVLNNGG KPRSFTLPRD  
851 SGFNHCCLNA PVSACDPQDD VQPPEVEEEE EEEEEEGEAA GENIGEKSES  
901 REEKLGDLSLQ DLYRALEQAS LSPLGEHRIS TKMEYKLSFI KRCNDPVMNE  
951 KLHRLRLKS TLKAREGEVA IIDKVLDNPD LTSKEFQQWK QMYLDLFLDI  
1001 CQNTTSNDPL SISSEVDVIT SSLAHTHSYI ETHV\*

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**Fig. 8: Alignment of SEQ ID NO. 1,  
human MAGUIN-1, with  
rat MAGUIN-1**

Length: 1034 aa

```

1  MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ  50
   ||||||||||||||||||||||||||||||||||||||||||||||||
1  MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ  50

51  ELEDLGVSRIGHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ  100
   ||||||||||||||||||||||||||||||||||||||||||||||||
51  ELEDLGVSRIGHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ  100

101 NFITGRRRRSGHYDGRTSRKLPNDFLTSTVVDLIGAAKSLLAWLDRSPFAAV  150
   ||||||||||||||||||||||||||||||||||||||||||||||||
101 NFITGRRRRSGHYDGRTSRKLPNDFLTSTVVDLIGAAKSLLAWLDRSPFAAV  150

151 TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTSLSGVCDHIIS  200
   ||||||||||||||||||||||||||||||||||||||||||||||||
151 TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTSLSGVCDHIIS  200

201 LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA  250
   ||||||||||||||||||||||||||||||||||||||||||||||||
201 LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA  250

251 DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLLKKRPQSM  300
   ||||||||||||||||||||||||||||||||||||||||||||||||
251 DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLLKKRPQSM  300

301 LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD  350
   ||||||||||||||||||||||||||||||||||||||||||||||||
301 LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD  350

351 LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR  400
   ||||||||||||||||||||||||||||||||||||||||||||||||
351 LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR  400

401 KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG  450
   ||||||||||||||||||||||||||||||||||||||||||||||||
401 KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG  450

451 DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKKG  500
   ||||||||||||||||||||||||||||||||||||||||||||||||
451 DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKKG  500

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```

501 DKSNSPTHYSLPQLMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK 550
   |||:|||||||||||||||||||||||||||||||||||||||||
501 DKSTSPTHYSLPQLMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK 550
   |||:|||||||||||||||||||||||||||||||||||||||||

551 NKGPIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD 600
   |||:|||||||||||||||||||||||||||||||||||||||||
551 NKGAIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD 600
   |||:|||||||||||||||||||||||||||||||||||||||||

601 ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA 650
   |||||||||||||||||||||||||||||||||||||||||||
601 ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA 650
   |||||||||||||||||||||||||||||||||||||||||||

651 AEHLDDMNRLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ 700
   |||||||||||||||||||||||||||||||||||||||||||
651 AEHLDDMNRLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ 700
   |||||||||||||||||||||||||||||||||||||||||||

701 DSPPPPYDTPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEV 750
   |||||||||||||||||||||||||||||||||||||||||||
701 DSPPPPYDTPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEV 750
   |||||||||||||||||||||||||||||||||||||||||||

751 GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSA 800
   |||||||||||||||||||||||||||||||||||||||||||
751 GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSA 800
   |||||||||||||||||||||||||||||||||||||||||||

801 SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNNGGKPRSFTLPR 850
   |||||||||||||||||||||||||||||||||||||||||||
801 SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNNGGKPRSFTLPR 850
   |||||||||||||||||||||||||||||||||||||||||||

851 SGFNHCCLNAPVSACDPQDDVQPPEVEEEEEEEEEEGEAAGENIGES 900
   ||||||||||||||||||||:||||||||||||||| |||||:|
851 SGFNHCCLNAPVSACDPQDDIQPPEVEEEEEEEEE..EAAGENIGEK 900
   ||||||||||||||||||||:||||||||||||||| |||||:|

901 REEKLGDLSLQDLYRALEQASLSPLGEHRISTKMEYKLSFIKRCNDP 950
   ||||||||||||||||||||:|||||||||||||||:|||||
901 REEKLGDLSLQDLYRALEQASLSPLGEHRISTKMEYKLSFIKRCNDP 950
   ||||||||||||||||||||:|||||||||||||||:|||||

951 KLHRLRILKSTLKAREGEVAIIDKVLDNPDLTSEFQQWKQMYLDLFL 1000
   |||||||||||||||||||||||||||||||||||||||||||
951 KLHRLRILKSTLKAREGEVAIIDKVLDNPDLTSEFQQWKQMYLDLFL 1000
   |||||||||||||||||||||||||||||||||||||||||||

999 CQNTTSNDPLSISSEVDVITSSLAHTHSYIETHV 1034
   ||||||||||||||||||||:|||||||||||||||
999 CQNTTSNDPLSISSEVDVITSSLAHTHSYIETHV 1034
   ||||||||||||||||||||:|||||||||||||||

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**Fig. 9: SEQ ID NO. 2: amino acid sequence of human MAGUIN-2 protein****Length: 898 aa**

1 MALIMEPVSK WSPSQVVDWM KGLDDCLQQY IKNFEREKIS GDQLLRITHQ  
51 ELEDLGVSRI GHQELILEAV DLLCALNYGL ETENLKTLSH KLNASAKNLQ  
101 NFITGRRRSG HYDGRTSRKL PNDFLTSVVD LIGAAKSLLA WLDRSPFAAV  
151 TDYSVTRNNV IQLCLELTTI VQQDCTVYET ENKILHVCKT LSGVCDHIIS  
201 LSSDPLVSQS AHLEVIQLAN IKPSEGLGMY IKSTYDGLHV ITGTTENSPA  
251 DRCKKIHAGD EVIQVNHQTV VGWQLKNLVN ALREDPSGVI LTLKKRPQSM  
301 LTSAPALLKN MRWKPLALQP LIPRSPTSSV ATPSSTISTP TKRDSSALQD  
351 LYIPPPPAEP YIPRDEKGNL PCEDLRGHMV GKPVHKGSES PNSFLDQEYR  
401 KRFNIVEEDT VLYCYEYEKG RSSSQGRRES TPTYGKLRPI SMPVEYNWVG  
451 DYEDPNKMKR DSRRENSLLR YMSNEKIAQE EYMFQRNSKK DTGKKSKKKG  
501 DKSNSPTHYS LLPSLQMDAL RQDIMGTPVP ETTLYHTFQQ SSLQHKSKKK  
551 NKGPIAGKSK RRISCKDLGR GDCEGWLWKK KDAKSYFSQK WKKYWFLKD  
601 ASLYWYINEE DEKAEGFISL PEFKIDRASE CRKKYAFKAC HPKIKSFYFA  
651 AEHLDDMNRW LNRINMLTAG YAERERIKQE QDYWSESDKE EADTPSTPKQ  
701 DSPPPPYDTY PRPPSMSCAS PYVEAKHSRL SSTETSQSQS SHEEFRQEV  
751 GSSAVSPIRK TASQRRSWQD LIETPLTSSG LHYLQTLPLE DSVFSDSAAI  
801 SPEHRRQSTL PTQKCHLQDH YGPYPLAESE RMQVLNGNGG KPRSFTLPRD  
851 SGFNHCCLNA PVSACDPQDD VQPPEVEEEE EEEEEEGEAA GENIGEKs\*

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**Figure 10: Alignment of SEQ ID NO. 2,  
human MAGUIN-2, with  
rat MAGUIN-2**

Length: 898 aa

```

1  MALIMEPVSKWSPSQVVDWMKGLDDCLQOYIKNFEREKISGDQLLRITHQ 50
  |||||||||||||||||||||||||||||||||||||||||||||||||||
1  MALIMEPVSKWSPSQVVDWMKGLDDCLQOYIKNFEREKISGDQLLRITHQ 50

51  ELEDLGVSRIHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ 100
  |||||||||||||||||||||||||||||||||||||||||||||||||||
51  ELEDLGVSRIHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ 100

101 NFITGRRRRSGHYDGRTSRKLPNDFLTSVVDLIGAASLLAWLDRSPFAAV 150
   |||||||||||||||||||||||||||||||||||||||||||||||||||
101 NFITGRRRRSGHYDGRTSRKLPNDFLTSVVDLIGAASLLAWLDRSPFAAV 150

151 TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS 200
   |||||||||||||||||||||||||||||||||||||||||||||||||||
151 TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS 200

201 LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA 250
   |||||||||||||||||||||||||||||||||||||||||||||||||||
201 LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA 250

251 DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLLKKRPQSM 300
   |||||||||||||||||||||||||||||||||||||||||||||||||||
251 DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLLKKRPQSM 300

301 LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD 350
   |||||||||||||||||||||||||||||||||||||||||||||||||||
301 LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD 350

351 LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR 400
   |||||||||||||||||||||||||||||||||||||||||||||||||||
351 LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR 400

401 KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG 450
   |||||||||||||||||||||||||||||||||||||||||||||||||||
401 KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG 450

451 DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKKG 500
   |||||||||||||||||||||||||||||||||||||||||||||||||||
451 DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKKG 500

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501 DKSNSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK 550
    |||:||||||||||||||||||||||||||||||||||||||||||
501 DKSTSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK 550

551 NKGPIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFLKD 600
    |||:||||||||||||||||||||||||||||||||||||||||||
551 NKGAIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFLKD 600

601 ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA 650
    ||||||||||||||||||||||||||||||||||||||||||||
601 ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA 650

651 AEHLDDMNRLNRLNMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ 700
    ||||||||||||||||||||||||||||||||||||||||||||
651 AEHLDDMNRLNRLNMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ 700

701 DSPPPPYDTPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEV 750
    ||||||||||||||||||||||||||||||||||||||||||||
701 DSPPPPYDTPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEV 750

751 GSSAVSPIRKTAQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI 800
    ||||||||||||||||||||||||||||||||||||||||||||
751 GSSAVSPIRKTAQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI 800

801 SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD 850
    ||||||||||||||||||||||||||||||||||||||||||||
801 SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD 850

851 SGFNHCCLNAPVSACDPQDDVQPPEVEEEEEEEEEEGEAAGENIGES 898
    |||||||||||||||:||||||| |||||||||
851 SGFNHCCLNAPVSACDPQDDIQPPEVEEEEEEEEE..EAAGENIGES 896

```

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**Fig. 11: SEQ ID NO. 3: nucleotide sequence of human MAGUIN-1 coding sequence**

Length: 3105 bp

```

1  ATGGCTCTGA  TAATGGAACC  GGTGAGCAAA  TGGTCTCCGA  GTCAAGTAGT  GGACTGGATG
61 AAAGGTCTTG  ATGACTGTTT  GCAGCAGTAT  ATTAAGAACT  TTGAGAGGGA  GAAGATCAGT
121 GGGGACCAGC  TGCTGCGCAT  TACACATCAG  GAGCTAGAAG  ATCTGGGGGT  CAGCCGCATT
181 GGCCATCAGG  AACTGATCTT  GGAAGCAGTT  GACCTTCTGT  GTGCATTGAA  TTATGGCTTG
241 GAAACAGAAA  ATCTAAAAAC  CCTTCTCAC  AAGTTGAATG  CATCTGCCAA  AAATCTGCAG
301 AATTTTATAA  CAGGAAGGAG  AAGGAGTGGC  CATTATGATG  GGAGGACCAG  CCGAAAATTG
361 CCAAACGACT  TTCTGACCTC  AGTTGTGGAT  CTGATTGGAG  CAGCCAAGAG  TCTGCTTGCC
421 TGGTTGGACA  GGTCACCATT  TGCTGCTGTG  ACAGACTATT  CAGTTACAAG  AAATAATGTC
481 ATACAAC'TCT  GCCTGGAGTT  AACAACAATT  GTGCAACAGG  ATTGTACTGT  ATATGAAACA
541 GAGAATAAAA  TTCTTCACGT  GTGTAAACT  CTTTCTGGAG  TCTGTGACCA  CATCATATCC
601 CTGTCGTGAG  ATCCTCTGGT  TTCACAGTCT  GCTCACCTGG  AAGTGATTCA  ACTGGCAAAC
661 ATTAACCAA  GCGAAGGGCT  GGGTATGTAT  ATTAATCTA  CATATGATGG  CCTCCATGTA
721 ATTACTGGAA  CCACAGAAAA  TTCACCTGCA  GATCGGTGCA  AGAAAATCCA  TGCTGGCGAT
781 GAAGTGATTC  AAGTTAATCA  TCAGACTGTG  GTGGGGTGGC  AGTTGAAAAA  TTTGGTGAAT
841 GCACTACGAG  AGGACCCGAG  TGGTGTATC  TTAAC'TTTGA  AAAAGCGACC  TCAGAGCATG
901 CTTACCTCAG  CACCAGCTTT  ACTGAAAAAT  ATGAGATGGA  AGCCCCTTGC  TCTGCAGCCT
961 CTTATACCTA  GAAGTCCAC  AAGCAGCGTT  GCCACGCCTT  CCAGCACCAT  CAGTACACCC
1021 ACCAAAAGAG  ACAGTTCTGC  CCTCCAGGAT  CTCTACATTC  CCCCTCCTCC  TGCAGAACCA
1081 TATAT'TCCCA  GGGATGAAAA  AGGAAACCTT  CCTTGTGAAG  ACCTCAGAGG  ACATATGGTG
1141 GGCAAGCCAG  TGCATAAGGG  ATCTGAATCA  CCAAATTCAT  TTCTGGATCA  GGAATATCGA
1201 AAGAGATTTA  ATATTGTCTGA  AGAAGATACT  GTCTTATATT  GCTATGAATA  TGAAAAAGGA
1261 AGATCAAGTA  GTCAAGGAAG  ACGAGAAAGC  ACCCCAAC'TT  ATGGCAAGCT  ACGACCTATA
1321 TCTATGCCAG  TGGAATATAA  TTGGGTGGGG  GACTATGAAG  ATCCAAATAA  GATGAAGAGA
1381 GATAGTAGAA  GAGAAAACTC  TCTACTTCGG  TATATGAGCA  ATGAAAAGAT  TGCTCAAGAA
1441 GAATACATGT  TTCAGAGAAA  CAGCAAAAAG  GACACAGGGA  AGAAGTCAAA  AAAGAAGGGT
1501 GATAAGAGTA  ATAGCCCAAC  TCACTATTCA  TTGCTACCTA  GTTTACAAAT  GGATGCACTG
1561 AGACAAGACA  TCATGGGCAC  TCCTGTGCCA  GAGACCACAC  TATACCATAC  ATTTTCAGCAG
1621 TCCTCACTGC  AGCACAAATC  AAAGAAGAAA  AACAAAGGTC  CTATAGCAGG  CAAGAGCAAA
1681 AGACGAATTT  CTTGCAAAGA  TCTTGCCCGT  GGTGACTGTG  AGGGCTGGCT  TTGAAAAAAG
1741 AAAGATCTGA  AGAGTTACTT  TTCACAGAAA  TGGAAAAAAT  ATTGGTTTGT  CCTAAAGGAT
1801 GCATCCCTTT  ATTGGTATAT  TAATGAGGAG  GATGAAAAAG  CAGAAGGATT  CATTAGCCTG
1861 CCTGAATTTA  AAATTGATAG  AGCCAGTGAA  TGCCGCAAAA  AATATGCATT  CAAAGCCTGT
1921 CATCCTAAAA  TCAAAAGCTT  TTATTTTGCT  GCTGAACATC  TTGATGATAT  GAACAGGTGG
1981 CTTAACAGAA  TTAATATGCT  GACTGCAGGA  TATGCAGAAA  GAGAGAGGAT  TAAGCAGGAA
2041 CAAGATTACT  GGAGTGAGAG  TGACAAGGAA  GAAGCAGATA  CTCCATCAAC  ACCAAAACAA
2101 GATAGCCCTC  CACCCCCATA  TGATACATAC  CCACGACCTC  CCTCGATGAG  TTGCGCCAGT
2161 CCTTATGTGG  AAGCAAAACA  TAGCCGACTT  TCCTCCACGG  AGACTTCTCA  GTCTCAGTCT
2221 TCTCATGAGG  AGTTTCGCCA  GGAAGTAACT  GGGAGCAGTG  CAGTGTCTCC  CATTGCAAG
2281 ACAGCCAGTC  AGCGCCGCTC  CTGGCAGGAT  TTAATTGAGA  CGCCACTGAC  AAGTTCAGGC
2341 TTACACTATC  TTCAGACTCT  GCCCCTGGAG  GATTCTGTCT  TCTCTGACTC  CGCGGCCATC
2401 TCCCCAGAGC  ACAGGCGGCA  GTCTACCCTG  CCAACTCAGA  AATGCCACCT  GCAGGATCAC
2461 TATGGGCCAT  ACCCCTTAGC  TGAGAGTGAG  AGGATGCAAG  TGCTAAATGG  AAATGGGGGC
2521 AAGCCTCGAA  GTTTTACTCT  GCCTCGAGAT  AGCGGGTTCA  ACCATTGCTG  TCTGAATGCT
2581 CCAGTTAGTG  CCTGTGACCC  ACAGGATGAC  GTGCAACCCC  CAGAGGTGGA  GGAAGAGGAG
2641 GAGGAGGAGG  AGGAGGAAGG  GGAGGCAGCA  GGGGAAAACA  TAGGAGAAAA  AAGTGAAAGC
2701 AGAGAAGAAA  AGTTAGGAGA  CTCATTGCAA  GATTTATACA  GGGCACTGGA  GCAGGCCAGT
2761 CTGTCACCAC  TAGGAGAACA  TCGTATTTCA  ACCAAGATGG  AATACAAGCT  ATCATTTATA
2821 AAAAGATGTA  ATGATCCTGT  AATGAATGAA  AAAC'TACACC  GGCTGAGATG  TCTCAAAAGC
2881 ACTTTAAAGG  CCAGAGAAGG  GGAAGTAGCC  ATTATCGATA  AAGTCCTAGA  ATATCCAGAC
2941 TTGACATCTA  AAGAATTCCA  ACAATGGAAG  CAGATGTACC  TCGACCTTTT  CTTGGATATC
3001 TGTCAAAATA  CCACCTCAAA  TGACCCACTG  AGTATTTCTT  CTGAAGTAGA  TGTAATCACT
3061 TCCTCTCTAG  CACACACTCA  TTCATACATT  GAAACGCATG  TCTAA

```

-14/26-

**Fig. 12: SEQ ID NO. 4: nucleotide sequence of human MAGUIN-2 coding sequence****Length: 2697 bp**

```

1   ATGGCTCTGA TAATGGAACC GGTGAGCAAA TGGTCTCCGA GTCAAGTAGT
51  GGACTGGATG AAAGGTCTTG ATGACTGTTT GCAGCAGTAT ATTAAGAACT
101 TTGAGAGGGA GAAGATCAGT GGGGACCAGC TGCTGCGCAT TACACATCAG
151 GAGCTAGAAG ATCTGGGGGT CAGCCGCATT GGCCATCAGG AACTGATCTT
201 GGAAGCAGTT GACCTTCTGT GTGCATTGAA TTATGGCTTG GAAACAGAAA
251 ATCTAAAAAC CCTTTCTCAC AAGTTGAATG CATCTGCCAA AAATCTGCAG
301 AATTTTATAA CAGGAAGGAG AAGGAGTGGC CATTATGATG GGAGGACCAG
351 CCGAAAATTG CCAAACGACT TTCTGACCTC AGTTGTGGAT CTGATTGGAG
401 CAGCCAAGAG TCTGCTTGCC TGGTTGGACA GGTCACCATT TGCTGCTGTG
451 ACAGACTATT CAGTTACAAG AAATAATGTC ATACAACCTC GCCTGGAGTT
501 AACAACAATT GTGCAACAGG ATTGTACTGT ATATGAAACA GAGAATAAAA
551 TTCTTCACGT GTGTAAAACT CTTTCTGGAG TCTGTGACCA CATCATATCC
601 CTGTCGTCAG ATCCTCTGGT TTCACAGTCT GCTCACCTGG AAGTGATTCA
651 GCTGGCAAAC ATTAAACCAA GCGAAGGGCT GGGTATGTAT ATTAAATCTA
701 CATATGATGG CCTCCATGTA ATTACTGGAA CCACAGAAAA TTCACCTGCA
751 GATCGGTGCA AGAAAAATCCA TGCTGGCGAT GAAGTGATTG AAGTTAATCA
801 TCAGACTGTG GTGGGGTGGC AGTTGAAAAA TTTGGTGAAT GCACTACGAG
851 AGGACCCGAG TGGTGTATAT TTAACCTTTG AAAAGCGACC TCAGAGCATG
901 CTTACCTCAG CACCAGCTTT ACTGAAAAAT ATGAGATGGA AGCCCCCTGC
951 TCTGCAGCCT CTTATACCTA GAAGTCCAC AAGCAGCGTT GCCACGCCCT
1001 CCAGCACCAT CAGTACACCC ACCAAAAGAG ACAGTTCTGC CCTCCAGGAT
1051 CTCTACATTC CCCCTCCTCC TGCAGAACCA TATATTCCCA GGGATGAAAA
1101 AGGAAACCTT CCTTGTGAAG ACCTCAGAGG ACATATGGTG GGCAAGCCAG
1151 TGCATAAGGG ATCTGAATCA CCAAATTCAT TTCTGGATCA GGAATATCGA
1201 AAGAGATTTA ATATTGTCTG AGAAGATACT GTCTTATATT GCTATGAATA
1251 TGAAAAAGGA AGATCAAGTA GTCAAGGAAG ACGAGAAAGC ACCCCAACCT
1301 ATGGCAAGCT ACGACCTATA TCTATGCCAG TGGAATATAA TTGGGTGGGG
1351 GACTATGAAG ATCCAAATAA GATGAAGAGA GATAGTAGAA GAGAAAACTC
1401 TCTACTTCGG TATATGAGCA ATGAAAAGAT TGCTCAAGAA GAATACATGT
1451 TTCAGAGAAA CAGCAAAAAG GACACAGGGA AGAAGTCAAA AAAGAAGGGT
1501 GATAAGAGTA ATAGCCCAAC TCACTATTCA TTGCTACCTA GTTTACAAAT
1551 GGATGCACTG AGACAAGACA TCATGGGCAC TCCTGTGCCA GAGACCACAC
1601 TATACCATAC ATTTCAGCAG TCCTCACTGC AGCACAAATC AAAGAAGAAA
1651 AACAAAGGTC CTATAGCAGG CAAGAGCAAA AGACGAATTT CTTGCAAGAA
1701 TCTTGGCCGT GGTGACTGTG AGGCTGGCT TTTGAAAAAG AAAGATGCGA
1751 AGAGTTACTT TTCACAGAAA TGGAAAAAAT ATTGGTTTGT CCTAAAGGAT
1801 GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT
1851 CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA
1901 AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT
1951 GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT
2001 GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT
2051 GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA
2101 GATAGCCCTC CACCCCATAT TGATACATAC CCACGACCTC CCTCGATGAG
2151 TTGCGCCAGT CTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG
2201 AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT
2251 GGGAGCAGTG CAGTGTCTCC CATTGCAAG ACAGCCAGTC AGCGCCGCTC
2301 CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC
2351 TTCAGACTCT GCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC
2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT
2451 GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG
2501 TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT
2551 AGCGGGTTCA ACCATTGCTG TCTGAaTGCT CCAGTTAGTG CCTGTGACCC
2601 ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG
2651 AGGAGGAAGG GGAGGCAGCA GGGGAAAAACA TAGGAGAAAA AAGCTAA

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**Fig. 13: SEQ ID NO. 5: nucleotide sequence of human MAGUIN-1 cDNA****Length: 5749 bp**

```

1  CGGGCAGCTA  GTCGTGCTCG  GGGCTTCACT  CCCGCGCGTG  AGGCGAGCGG  GCAAGTTGGC
61  TGAGGGCGTG  CGGCAGAGGC  TGCTTCCCTC  GGCGACGCGA  CCCCTCAGCA  ACTCAAGCTA
121  TGAAGTGAAG  CTCCCTAGGG  ACGGAGACCG  GAGCGGAGCG  GCGGAGGCAG  CAGCAGCAGC
181  AGCAGCAGCA  GCAGCAGCAG  CAGCCGCCGC  CGCCGCCGCC  TTAGCGGGAA  CTGAGCAGAC
241  CCGGCGCGGA  GCCACGACTC  CTGCACGTTT  ACCTCCCTGT  CGCCGTTCTT  GCCGGCGGTT
301  GGCTAAAAGA  CGTTACAGCC  GCGAGACCCG  ACACACAAAA  GCCGCTTCTT  CCGCGCCGCC
361  CGCCAGGGA  GGTGCGGCC  AGCAAGGGAC  CCCACCTGAG  AGCAGCTCGG  GCTGCTGAGT
421  TCGTTTTGTG  TCTGAGCTCT  GCGCTCTGCA  CGGAACCGAC  CCCGTACCCA  TGGCTCTGAT
481  AATGGAACCG  GTGAGCAAAT  GGTCTCCGAG  TCAAGTAGTG  GACTGGATGA  AAGGTCTTGA
541  TGACTGTTTG  CAGCAGTATA  TTAAGAACTT  TGAGAGGGAG  AAGATCAGTG  GGGACCAGCT
601  GCTGCGCATT  ACACATCAGG  AGCTAGAAGA  TCTGGGGGTC  AGCCGCATTG  GCCATCAGGA
661  ACTGATCTTG  GAAGCAGTTG  ACCTTCTGTG  TGCATTGAAT  TATGGCTTGG  AAACAGAAAA
721  TCTAAAAACC  CTTTCTCACA  AGTTGAATGC  ATCTGCCAAA  AATCTGCAGA  ATTTTATAAC
781  AGGAAGGAGA  AGGAGTGGCC  ATTATGATGG  GAGGACCAGC  CGAAAATTGC  CAAACGACTT
841  TCTGACCTCA  GTTGTGGATC  TGATTGGAGC  AGCCAAGAGT  CTGCTTGCCCT  GGTGGGACAG
901  GTCACCATTT  GCTGCTGTGA  CAGACTATTC  AGTTACAAGA  AATAATGTCA  TACAACCTTG
961  CCTGGAGTTA  ACAACAATTG  TGCAACAGGA  TTGTACTGTA  TATGAAACAG  AGAATAAAAT
1021  TCTTCACGTG  TGTAAAACTC  TTTCTGGAGT  CTGTGACCAC  ATCATATCCC  TGTCGTCAGA
1081  TCCTCTGGTT  TCACAGTCTG  CTCACCTGGA  AGTGATTCAA  CTGGCAAACA  TTAAACCAAG
1141  CGAAGGGCTG  GGTATGTATA  TTAAATCTAC  ATATGATGGC  CTCCATGTAA  TTACTGGAAC
1201  CACAGAAAAT  TCACCTGCAG  ATCGGTGCAA  GAAAATCCAT  GCTGGCGATG  AAGTGATTCA
1261  AGTTAATCAT  CAGACTGTGG  TGGGGTGGCA  GTTGAAAAAT  TTGGTGAATG  CACTACGAGA
1321  GGACCCGAGT  GGTGTTATCT  TAACTTTGAA  AAAGCGACCT  CAGAGCATGC  TTACCTCAGC
1381  ACCAGCTTTA  CTGAAAAATA  TGAGATGGAA  GCCCCTTGCT  CTGCAGCCTC  TTATACCTAG
1441  AAGTCCCACA  AGCAGCGTTG  CCACGCCTTC  CAGCACCATC  AGTACACCCA  CCAAAGAGA
1501  CAGTTCTGCC  CTCAGGATC  TCTACATTCC  CCCTCCTCCT  GCAGAACCAT  ATATTCCCAG
1561  GGATGAAAAA  GGAAACCTTC  CTTGTGAAGA  CCTCAGAGGA  CATATGGTGG  GCAAGCCAGT
1621  GCATAAGGGA  TCTGAATCAC  CAAATTCATT  TCTGGATCAG  GAATATCGAA  AGAGATTTAA
1681  TATTGTGCGA  GAAGATACTG  TCTTATATTG  CTATGAATAT  GAAAAAGGAA  GATCAAGTAG
1741  TCAAGGAAGA  CGAGAAAGCA  CCCCAACTTA  TGGCAAGCTA  CGACCTATAT  CTATGCCAGT
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1921  TCAGAGAAAC  AGCAAAAAGG  ACACAGGGAA  GAAGTCAAAA  AAGAAGGGTG  ATAAGAGTAA
1981  TAGCCCAACT  CACTATTCAT  TGCTACCTAG  TTTACAAATG  GATGCACTGA  GACAAGACAT
2041  CATGGGCACT  CCTGTGCCAG  AGACCACACT  ATACCATACA  TTTCAGCAGT  CCTCACTGCA
2101  GCACAAATCA  AAGAAGAAAA  ACAAAGGTCC  TATAGCAGGC  AAGAGCAAAA  GACGAATTTT
2161  TTGCAAAAGAT  CTTGGCCGTG  GTGACTGTGA  GGGCTGGCTT  TGGAAAAAGA  AAGATGCGAA
2221  GAGTTACTTT  TCACAGAAAT  GGAAAAATA  TTGGTTTGTC  CTAAAGGATG  CATCCCTTTA
2281  TTGGTATATT  AATGAGGAGG  ATGAAAAAGC  AGAAGGATTC  ATTAGCCTGC  CTGAATTTAA
2341  AATTGATAGA  GCCAGTGAAT  GCCGCAAAAA  ATATGCATTG  AAAGCCTGTC  ATCCTAAAAT
2401  CAAAAGCTTT  TATTTTGCTG  CTGAACATCT  TGATGATATG  AACAGGTGGC  TTAACAGAAT
2461  TAATATGCTG  ACTGCAGGAT  ATGCAGAAAG  AGAGAGGATT  AAGCAGGAAC  AAGATTACTG
2521  GAGTGAGAGT  GACAAGGAAG  AAGCAGATAG  TCCATCAACA  CCAAAACAAG  ATAGCCCTCC
2581  ACCCCCATAT  GATACATACC  CACGACCTCC  CTCGATGAGT  TGCGCCAGTC  CTTATGTGGA
2641  AGCAAAACAT  AGCCGACTTT  CCTCCACGGA  GACTTCTCAG  TCTCAGTCTT  TCTATGAGGA
2701  GTTTCGCCAG  GAAGTAAC TG  GGAGCAGTGC  AGTGTCTCCC  ATTCGCAAGA  CAGCCAGTCA
2761  GCGCCGCTCC  TGGCAGGATT  TAATTGAGAC  GCCACTGACA  AGTTCAGGCT  TACACTATCT
2821  TCAGACTCTG  CCCCTGGAGG  ATTCTGTCTT  CTCTGACTCC  GCGGCCATCT  CCCCAGAGCA

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2881 CAGGCGGCAG TCTACCCTGC CAACTCAGAA ATGCCACCTG CAGGATCACT ATGGGCCATA  
 2941 CCCCTTAGCT GAGAGTGAGA GGATGCAAGT GCTAAATGGA AATGGGGGCA AGCCTCGAAG  
  
 3001 TTTTACTCTG CCTCGAGATA GCGGGTTCAA CCATTGCTGT CTGAATGCTC CAGTTAGTGC  
 3061 CTGTGACCCA CAGGATGACG TGCAACCCCC AGAGGTGGAG GAAGAGGAGG AGGAGGAGGA  
 3121 GGAGGAAGGG GAGGCAGCAG GGGAAAACAT AGGAGAAAAA AGTGAAAGCA GAGAAGAAAA  
 3181 GTTAGGAGAC TCATTGCAAG ATTTATACAG GGCCTGGAG CAGGCCAGTC TGTCACCACT  
 3241 AGGAGAACAT CGTATTTCAA CCAAGATGGA ATACAAGCTA TCATTTATAA AAAGATGTAA  
 3301 TGATCCTGTA ATGAATGAAA AACTACACCG GCTGAGAATT CTCAAAGCA CTTTAAAGGC  
 3361 CAGAGAAGGG GAAGTAGCCA TTATCGATAA AGTCCTAGAC AATCCAGACT TGACATCTAA  
 3421 AGAATTCCAA CAATGGAAGC AGATGTACCT CGACCTTTTC TTGGATATCT GTCAAAATAC  
 3481 CACCTCAAAAT GACCCACTGA GTATTTCTTC TGAAGTAGAT GTAATCACTT CCTCTCTAGC  
 3541 ACACACTCAT TCATACATTG AAACGCATGT CTAAATGTAT TCTGCCTTCA GACCATCTAG  
 3601 TACCTGCTGG TACTCTGAAC AAGTATATAA GGTAGTTTTT ATATCAATGT GTGGAACACT  
 3661 TGACAAGCTA TACTTTAATG TTACCAAACAT ATATGAAACA AACCATATAT GGTCAACAATA  
 3721 CCACTATCTT TAATGAGCAT TTGTATATTT TATATGCAAC AGTGCTCAGC TTATGTTTAC  
 3781 CATGTGCAAA ATCAACTGTC TTTAATGACT TAAATTAAC TTTTGCAAAAC AATTCTAAAT  
 3841 ACAGGTGGTC TTCAAGTAGT AAAACCACAA AAGGCAGTTT TCTATCTATG GTCATCTTTT  
 3901 CTCCCTTTAA GTTAATTTTA TATAACAAG ACTTCAAAAAG TAAATCACAT TTTTTCAGGT  
 3961 GCAGACATCC TTGTGGGTGG GAAAGAATTT AAACCTTTTT TATATTTATT AAAATGTTCT  
 4021 AAGAATTTTC TTAAACATTG CACAAAGTTT AATGCTGTAG TTTTATTTTT GTGAAATGTA  
 4081 GATGCGCATA CAAGAGCTAA GCAAAATAGA AGAGCATCGA CATAAGAAAA GTTCAGGTAT  
 4141 CTAATATTCG TCTTAATAGT CTATTAACCT GTGAAAGCTA AGTTAATGGA AATATTATTC  
 4201 CAAATCTATG AGAACACTTG GTGTATCAGG GCAAAGCTTT GTAAGATGTT TTTGTAACATA  
 4261 AGACCAAAAT TGAAGATAGA GCTGCTTTAT TTTCTTGGTT TAAATCTTCC TTTATTTTTG  
 4321 TAGTGATGAG ATGCTGATTG TGTACAGAAG AATTGAGAG GGGATTTTTA AAAACTGACT  
 4381 TAACACACCC AGAAAGGCAG CTAACAGCTA TATATATATA TAAATTTTCAG CCCAAACTCA  
 4441 TGTTTTAAA CTCCAACCTC TAAAAGACAA CAAGGTATAA ACTGAAATGA ATCAACTTTC  
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 4561 AGGGAAGTAC AATATGTTTA GTTTCAGGCT GATGTGTGTT ATAAAAACA ACACTGAAAA  
 4621 ATAAAAATGT ACTTCCCTTC TAAGGAGCAA GCAGGTGATG GTCATTCAA GAGATGTCAC  
 4681 ATTGAATTAT GAGAGAAACA ATTTAGAGGT TTTTTCCTG GCTTCATGAA TTGTTCTATA  
 4741 GAGTGGATGA AGTCTAAGGA AAAGTCCTCT TCATATATTT CCATTTATAA GCGTCTTGTT  
 4801 TTTGAAAAGTG ATCACAGCAT GAAAATGACT GTGCTGCTTT TTAGTGTCTG GCTGCATAAT  
 4861 GTACAAGTCA CAATTTGCTG TTTTTTTCAG GAGGAGAAAG GGAACCTCCT TTACTATTCT  
 4921 ATATCCTAAA ATCTACTTCT AATCAGCTTT ATACTGTTGC CTGTACAGCT CAGTGAATGT  
 4981 ACTTTCATCT TTAAGAGTTC AGATATATGC CAGTGAATAT TTTTGCTGTA GAGGAGAAAG  
 5041 TAAAAACTCC ACAGCGGGGA TCTTTTCTT TGCTTTTGAA ACCACCATG AATCACTATC  
 5101 GTTTTGACAGA CTTTGCACAA CTGTACAGGA GAGTGGCCTT TCTACAGCAC ATTTTCAGTA  
 5161 ATCCTATATT TAGTCAAAAT GGATGAGAAA TCATGTATTA ATGTTTGTAT GGAATTTTGG  
 5221 GTCCAGTGTA ATATTTTAT CATTAAAAA GAACCTCTAT TGTA AAAACA TTTATTTACT  
 5281 GCATGGATAT TGACGCACAT TAAATTTGTG GGATTTTGTA TATGTAAAAA AAAAAAAAAA  
 5341 AAAAAAAAAAC AAAAAACCTC TTGTCTAAA ATGAAGTGTG CTTGTAAACA GGTGTTTAGA  
 5401 CTTATTGATG TTTACTAGAC CAAATGTGTA TGTTCACTTA AAAATATATG TACCTGATGG  
 5461 ATGTGTCATG TTTACAGTGG CCAGTTGTG GCCTGTAAAC AGCAAGCAGT TGACGGGAAG  
 5521 ACTAGCTCTG TTGCTACTAA GCAGCTTTTA CTTTGTAAA GTGAGCTCTG TTGTTTTAAA  
 5581 TGGTAAAAAT TAACTAATG AATTTGACAA GACTCGTGGC TAGCCTAGCA TGAAAGAGAC  
 5641 CTTTTAACAC TATATAATAT CTGTACATTT TATTGCATTC GTTTCAAATC TAGGAGAGAG  
 5701 GCAGCACTGT AAACGAAGT CAAATAAATT CAGCTCTTAA TGAATCCTT

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**Fig. 14: SEQ ID NO. 6: nucleotide sequence of human MAGUIN-2 cDNA****Length: 4350 bp**

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1  GTGCTCGGGG CTTCACTCCC GCGCGTGAGG CGAGCGGGCA AGTTGGCTGA
51  GGGCGTGCGG CAGAGGCTGC TTCCCTCGGC GACGCGACCC CTCAGCAACT
101 CAAGCTATGA ACTGAAGCTC CCTAGGGACG GAGACCGGAG CGGAGCGGCG
151 GAGGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CCGCCGCCGC
201 CGCCGCCTTA GCGGGAAC TG AGCAGACCCG GCGCGGAGCC ACGACTCCTG
251 CACGTTTACC TCCCTGTTCG CGTTTCTGCC GCGCGTTGGC TAAAAGACGT
301 TACAGCCGCG AGACCCGACA CACAAAAGCC GCTTTCTCCG CGCCGCCCGC
351 CCAGGGAGGC TCGGCCAGC AAGGGACCCC ACCTGAGAGC AGCTCGGGCT
401 GCTGAGTTCG TTTTGTGTCT GAGCTCTGCG CTCTGCACGG AACCGACCCC
451 GTACCCATGG CTCTGATAAT GGAACCGGTG AGCAAATGGT CTCCGAGTCA
501 AGTAGTGGAC TGGATGAAAG GTCTTGATGA CTGTTTGCAG CAGTATATTA
551 AGAACTTTGA GAGGGAGAAG ATCAGTGGGG ACCAGCTGCT GCGCATTACA
601 CATCAGGAGC TAGAAGATCT GGGGGTCAGC CGCATTGGCC ATCAGGAACT
651 GATCTTGGA GAGTTGACC TTCTGTGTGC ATTGAATTAT GGCTTGGA
701 CAGAAAATCT AAAAACCCCT TCTCACAAGT TGAATGCATC TGCCAAAAAT
751 CTGCAGAATT TTATAACAGG AAGGAGAAGG AGTGGCCATT ATGATGGGAG
801 GACCAGCCGA AAATTGCCAA ACGACTTTCT GACCTCAGTT GTGGATCTGA
851 TTGGAGCAGC CAAGAGTCTG CTTGCCTGGT TGGACAGGTC ACCATTGCT
901 GCTGTGACAG ACTATTCAGT TACAAGAAAT AATGTCATAC AACTTGCCT
951 GGAGTTAACA ACAATTGTGC AACAGGATTG TACTGTATAT GAAACAGAGA
1001 ATAAAATTCT TCACGTGTGT AAAACTCTTT CTGGAGTCTG TGACCACATC
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1101 GATTCAGCTG GCAAACATTA AACCAAGCGA AGGGCTGGGT ATGTATATTA
1151 AATCTACATA TGATGGCCTC CATGTAATTA CTGGAACCAC AGAAAATTCA
1201 CCTGCAGATC GGTGCAAGAA AATCCATGCT GGCGATGAAG TGATTCAAGT
1251 TAATCATCAG ACTGTGGTGG GGTGGCAGTT GAAAAATTTG GTGAATGCAC
1301 TACGAGAGGA CCCGAGTGGT GTTATCTTAA CTTTGAAAAA GCGACCTCAG
1351 AGCATGCTTA CCTCAGCACC AGCTTTACTG AAAAAATATG ATGGAAGCC
1401 CCTTGCTCTG CAGCCTCTTA TACCTAGAAG TCCCAACAAG AGCGTTGCCA
1451 CGCCTTCCAG CACCATCAGT ACACCCACCA AAAGAGACAG TTCTGCCCTC
1501 CAGGATCTCT ACATTCCCCC TCCTCCTGCA GAACCATATA TTCCCAGGGA
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1601 AGCCAGTGCA TAAGGGATCT GAATCACCAA ATTCATTTCT GGATCAGGAA
1651 TATCGAAAGA GATTTAATAT TGTGAAGAA GATACTGTCT TATATTGCTA
1701 TGAATATGAA AAAGGAAGAT CAAGTAGTCA AGGAAGACGA GAAAGCACCC
1751 CAACTTATGG CAAGCTACGA CCTATATCTA TGCCAGTGGA ATATAATTGG
1801 GTGGGGGACT ATGAAGATCC AAATAAGATG AAGAGAGATA GTAGAAGAGA
1851 AAACCTCTTA CTTCCGTATA TGAGCAATGA AAAGATTGCT CAAGAAGAAT
1901 ACATGTTTCA GAGAAACAGC AAAAAGGACA CAGGGAAGAA GTCAAAAAAG
1951 AAGGGTGATA AGAGTAATAG CCCAACTCAC TATTCATTGC TACCTAGTTT
2001 ACAAATGGAT GCACTGAGAC AAGACATCAT GGGCACTCCT GTGCCAGAGA
2051 CCACACTATA CCATACATTT CAGCAGTCCT CACTGCAGCA CAAATCAAAG
2101 AAGAAAAACA AAGGTCCAT AGCAGGCAAG AGCAAAAGAC GAATTTCTTG
2151 CAAAGATCTT GGCCGTGGTG ACTGTGAGGG CTGGCTTTGG AAAAAGAAAG
2201 ATGCGAAGAG TTACTTTTCA CAGAAATGGA AAAAATATTG GTTTGTCCCTA
2251 AAGGATGCAT CCCTTTATTG GTATATTAAT GAGGAGGATG AAAAAGCAGA

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2301 AGGATTCATT AGCCTGCCTG AATTTAAAAT TGATAGAGCC AGTGAATGCC  
 2351 GCAAAAAATA TGCATTCAAA GCCTGTCTATC CTAAAAATCAA AAGCTTTTAT  
  
 2401 TTTGCTGCTG AACATCTTGA TGATATGAAC AGGTGGCTTA ACAGAATTAA  
 2451 TATGCTGACT GCAGGATATG CAGAAAGAGA GAGGATTAAG CAGGAACAAG  
 2501 ATTACTGGAG TGAGAGTGAC AAGGAAGAAG CAGATACTCC ATCAACACCA  
 2551 AAACAAGATA GCCCTCCACC CCCATATGAT ACATACCCAC GACCTCCCTC  
 2601 GATGAGTTGC GCCAGTCCTT ATGTGGAAGC AAAACATAGC CGACTTTCTT  
 2651 CCACGGAGAC TTCTCAGTCT CAGTCTTCTC ATGAGGAGTT TCGCCAGGAA  
 2701 GTAAC TGGGA GCAGTGCAGT GTCTCCCATC CGCAAGACAG CCAGTCAGCG  
 2751 CCGCTCCTGG CAGGATTTAA TTGAGACGCC ACTGACAAGT TCAGGCCTTAC  
 2801 ACTATCTTCA GACTCTGCCC CTGGAGGATT CTGTCTTCTC TGACTCCGCG  
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 2951 TGCAAGTGCT AAATGGAAAT GGGGGCAAGC CTCGAAGTTT TACTCTGCCT  
 3001 CGAGATAGCG GGTTCACCA TTGCTGTCTG AaTGCTCCAG TTAGTGCCTG  
 3051 TGACCCACAG GATGACGTGC AACCCCCAGA GGTGGAGGAA GAGGAGGAGG  
 3101 AGGAGGAGGA GGAAGGGGAG GCAGCAGGGG AAAACATAGG AGAAAAAAGC  
 3151 TAATACACTG CGAGAGTTGG TAGAACCTCT CCATGCCAAA TCGGATCCAC  
 3201 TTCTGTTGGC ACTCAACCCA TTGGACTCAC AGATTGATAA GCTAATGTTT  
 3251 AGAGAAATTTA GATCGGAGAG AGTCGGTACG GCGCAGACTC AACATCAACC  
 3301 TCTTGCAAGC AACTAAAATG GCCTCGTCCT TGCTGTTTAT AACAGAAAAC  
 3351 AGACTTGTA AAAGCTTAGA TCATCAAGTG TTTTGATTG GGGGCCTCCC  
 3401 AAAGGGATAT AAGAGGGGCA GGCCACTCTT AAGAAGAATG CGAGCTTTCT  
 3451 ACATTGGGAC TAGCATAAGA TCAAAGCCAA TCAAGATGGA GCACAGTAAC  
 3501 AGAAAAC TGC GGTTCCTGTG GGAGAACAGA AGGGGAAAGG GTCTTAAC TGC  
 3551 GGAAAGGGCT CTGTGTGGTA ACACCTCAGT TGTGTTCTCC TGACACCAGG  
 3601 AAAAGAGAGG GATCAGCTTC AATAACTAGA AAATCTGTC TGTTTAATGG  
 3651 ACTCTTTGGT GGCCTCTTTA AGGCAAAGCA GAGAAAGCAA ATTATGTATT  
 3701 AAGTGTATTT TGCATTTTTA AAACCTTGACG TGCTGTATTG TACTAAATTA  
 3751 AGTGTAATCT ATTAAGGCAA GGTATACACA ATTTGCTTTG AAACCTTACTA  
 3801 TGTTTATTCT ATTATAAAGT GTATTCAGGT GCAACACAGA GACTGCTTTC  
 3851 GGTGACATTA ATGAAGAAAA TTTCTCATGC CAGGCTTTAT TATAGAATCT  
 3901 TCAGCTAAAA TCCTAACTTT CTCCTTATTT CTGGCACTT GTATACAAGT  
 3951 GGTGTTGCCT CTTAGGGCAG GCATGAGCTA TTCTTTTCTG TAAAATATTT  
 4001 TGAATCTATA GGCTGTGGGT TTCATTTTTG AAAAGTATTT TGTCTGGATG  
 4051 TCTTTCAAAC TAGCTTCAGA TATTATTTAA TACTATGTAA CTGGGTCCCC  
 4101 TATGGCTCAA TCAATATTGC TTATTTTCT TCTGTAGTGG ATGTGAAATT  
 4151 TCCTTTAGTT GGATAAGATA CACTGTAATA ATTTTAATGC TAATTAATGA  
 4201 TATTTTCATAC TGTGCAATGA ACAGATAATT TAACACTGTA TTTTGAAATG  
 4251 TTTTTTCTT CCTGTCACCG CAGTGTGTGG TATTGCATAA TGTGAATACC  
 4301 TGTA AAAATA TAAATTACTT AAAAATAAAA ATATGACCAA TTGGTATCAG

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**Figure 15: SEQ ID NO. 7**

**Length: 50 bp**

1 GGAGAGAGGCAGCACTGTAACTGAAGTCAAATAAATTCAGCTCTTAATG

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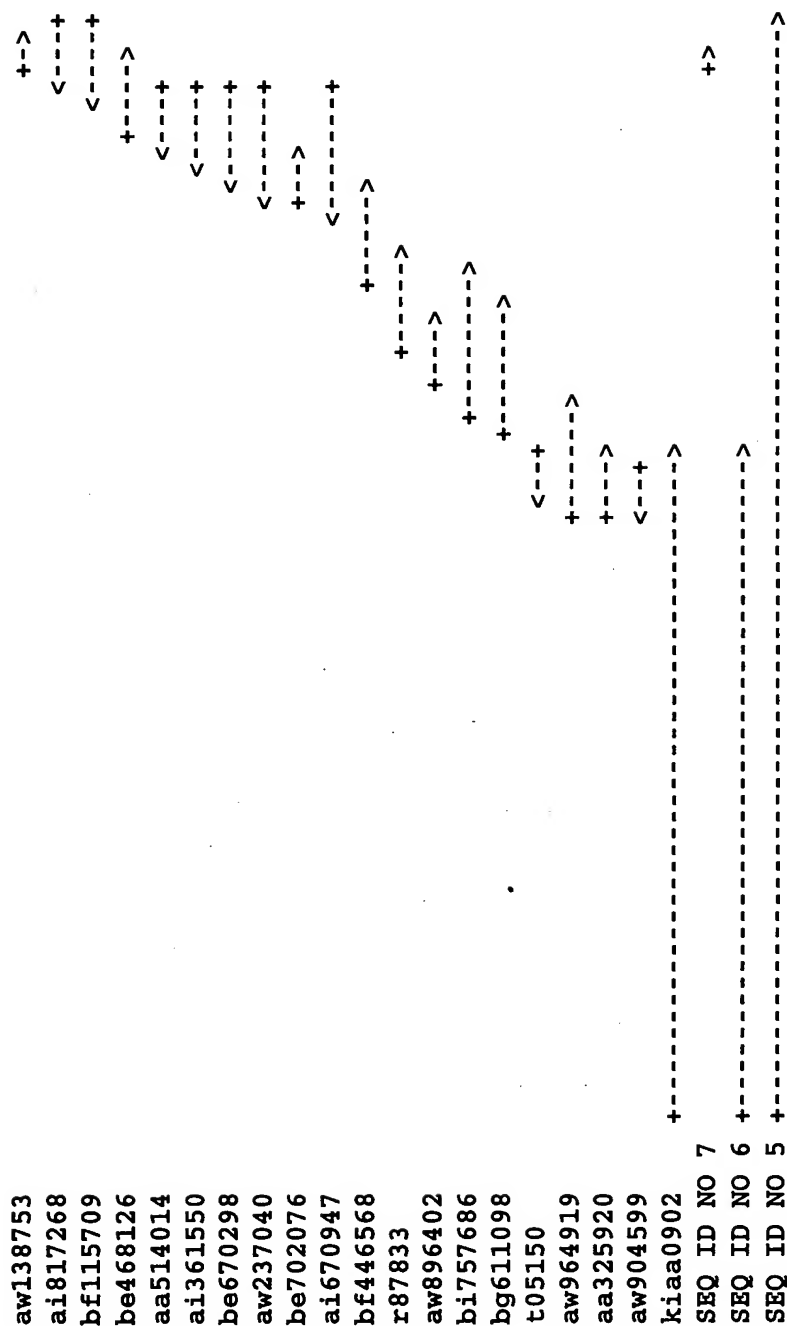
**Fig. 16: Alignment of SEQ ID NO. 7  
with human MAGUIN-1 cDNA**

Length: 50 bp

```
1 GGAGAGAGGCAGCACTGTAACTGAAGTCAAATAAATTCAGCTCTTAATG 50
  |||
5693 GGAGAGAGGCAGCACTGTAACTGAAGTCAAATAAATTCAGCTCTTAATG 5742
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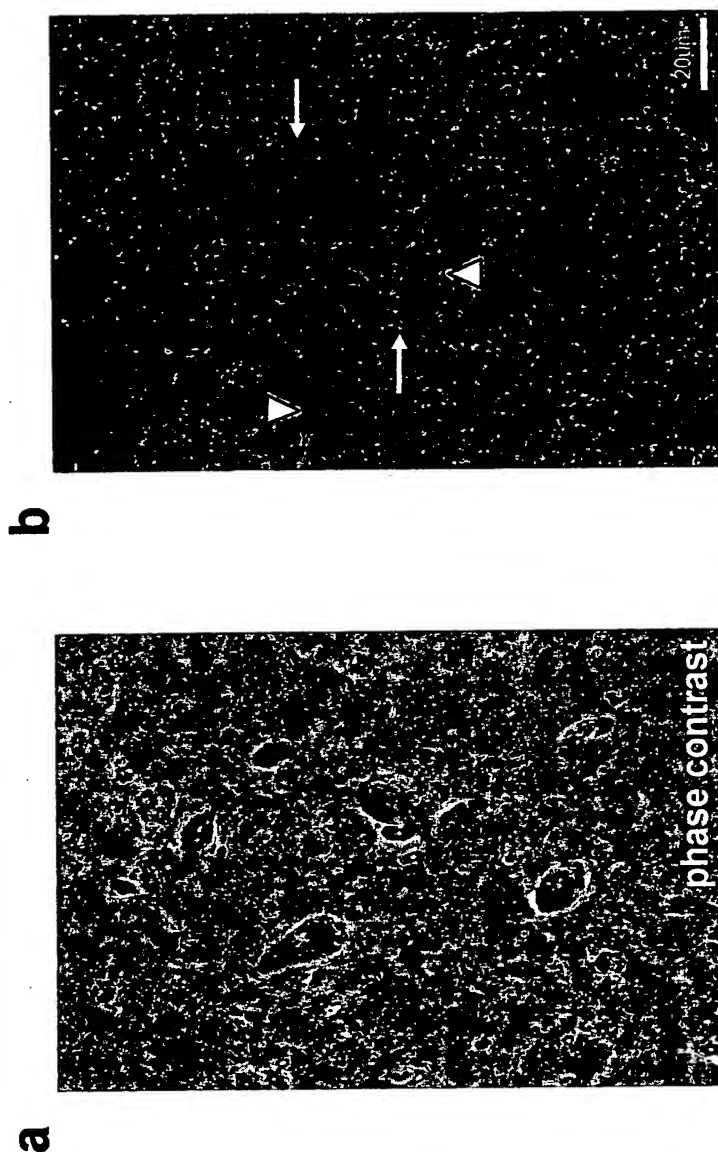
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**Fig. 17: Schematic alignment of SEQ ID NO. 5,  
SEQ ID NO. 6 and SEQ ID NO. 7 with  
Genome Database EST-cluster**



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**Fig. 18: Images of the human cerebral cortex  
labeled with anti-Maguin-1 antiserum  
and with DAPI**



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**Table 1:**

<b>sample</b>	<b><math>\Delta</math> (fold)</b> (frontal / temporal cortex)
patient P012	2.46
patient P016	2.78
patient P010	4.14
patient P011	2.20
patient P014	1.48
patient P017	1.42
patient P019	1.68
control C011	1.28
control C012	1.29
control C014	0.30
control C005	1.36
control C008	1.15

**Table 2:**

sample	$\Delta$ (fold) (frontal cortex / hippocampus)
patient P012	1.37
patient P016	3.07
patient P010	2.99
patient P011	2.28
patient P014	1.21
patient P019	1.48
control C005	1.74
control C008	0.39
control C004	0.87

**Table 3:**

sample	$\Delta$ (fold) (frontal / temporal cortex)
<hr/>	
patient P012	2.68
patient P016	2.72
patient P010	11.73
patient P011	2.44
patient P014	1.77
patient P017	3.43
patient P019	4.02
control C011	1.42
control C012	1.22
control C014	0.30
control C005	0.92
control C008	0.81

**Table 4:**

<b>sample</b>	<b><math>\Delta</math> (fold)</b> <b>(frontal cortex / hippocampus)</b>
patient P012	1.57
patient P016	4.38
patient P010	9.08
patient P011	4.53
patient P014	0.72
patient P019	1.37
control C005	1.84
control C008	0.46
control C004	1.69

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